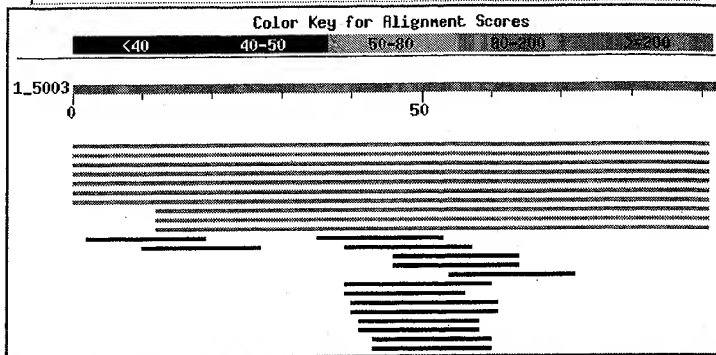


Part of the  
office action

attachment for sequencing search

**Distribution of 25 Blast Hits on the Query Sequence**

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

Score E  
(bits) Value

<a href="#">gi 24054235 gb AE015383.1 </a>	Shigella flexneri 2a str. 301 se...	<u>182</u>	6e-44
<a href="#">gi 30043176 gb AE016991.1 </a>	Shigella flexneri 2a str. 2457T ...	<u>182</u>	6e-44

<a href="#">gi 2367266 gb AE000447.1 AE000447</a>	Escherichia coli K12 MG16...	<a href="#">182</a>	<a href="#">6e-44</a>
<a href="#">gi 290484 gb L10328.1 ECOUW82</a>	E. coli; the region from 81.5...	<a href="#">182</a>	<a href="#">6e-44</a>
<a href="#">gi 12518536 gb AE005601.1 AE005601</a>	Escherichia coli O157:H7...	<a href="#">174</a>	<a href="#">1e-41</a>
<a href="#">gi 13363930 dbj AP002566.1 </a>	Escherichia coli O157:H7 DNA, c...	<a href="#">174</a>	<a href="#">1e-41</a>
<a href="#">gi 26110701 gb AE016769.1 </a>	Escherichia coli CFT073 section ...	<a href="#">167</a>	<a href="#">4e-39</a>
<a href="#">gi 29139451 gb AE016846.1 </a>	Salmonella enterica subsp. enter...	<a href="#">111</a>	<a href="#">2e-22</a>
<a href="#">gi 16504729 emb AL627280.1 </a>	Salmonella enterica serovar Typ...	<a href="#">111</a>	<a href="#">2e-22</a>
<a href="#">gi 16422410 gb AE008879.1 </a>	Salmonella typhimurium LT2, sect...	<a href="#">103</a>	<a href="#">5e-20</a>
<a href="#">gi 14589682 gb AC020589.4 </a>	Homo sapiens BAC clone RP11-143G...	<a href="#">38</a>	<a href="#">2.2</a>
<a href="#">gi 24202118 gb AE011592.1 </a>	Leptospira interrogans serovar l...	<a href="#">38</a>	<a href="#">2.2</a>
<a href="#">gi 17739388 gb AE009065.1 AE009065</a>	Agrobacterium tumefaciens...	<a href="#">38</a>	<a href="#">2.2</a>
<a href="#">gi 15156031 gb AE008032.1 AE008032</a>	Agrobacterium tumefaciens...	<a href="#">38</a>	<a href="#">2.2</a>
<a href="#">gi 14193024 gb AC013718.6 </a>	Homo sapiens BAC clone RP11-116I...	<a href="#">38</a>	<a href="#">2.2</a>
<a href="#">gi 19909496 gb AC098742.4 </a>	Mus musculus BAC clone RP23-122N...	<a href="#">36</a>	<a href="#">8.8</a>
<a href="#">gi 33147141 gb AC144644.3 </a>	Medicago truncatula clone mth2-1...	<a href="#">36</a>	<a href="#">8.8</a>
<a href="#">gi 18642908 gb AC080132.6 </a>	Homo sapiens BAC clone RP11-166B...	<a href="#">36</a>	<a href="#">8.8</a>
<a href="#">gi 29243387 dbj AP001011.6 </a>	Homo sapiens genomic DNA, chrom...	<a href="#">36</a>	<a href="#">8.8</a>
<a href="#">gi 29243373 dbj AP005061.3 </a>	Homo sapiens genomic DNA, chrom...	<a href="#">36</a>	<a href="#">8.8</a>
<a href="#">gi 13810526 dbj AP000923.5 </a>	Homo sapiens genomic DNA, chrom...	<a href="#">36</a>	<a href="#">8.8</a>
<a href="#">gi 15787722 emb AL162574.14 </a>	Human DNA sequence from clone ...	<a href="#">36</a>	<a href="#">8.8</a>
<a href="#">gi 16944202 emb AL603792.12 </a>	Mouse DNA sequence from clone ...	<a href="#">36</a>	<a href="#">8.8</a>
<a href="#">gi 15128594 dbj AB055625.1 </a>	Inversidens japonensis mitochon...	<a href="#">36</a>	<a href="#">8.8</a>
<a href="#">gi 14043054 emb AL450324.10 </a>	Human DNA sequence from clone ...	<a href="#">36</a>	<a href="#">8.8</a>

#### Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|24054235|gb|AE015383.1|](#) ☒ Shigella flexneri 2a str. 301 section 346 of 412 o  
genome  
Length = 10768

Score = 182 bits (92), Expect = 6e-44  
Identities = 92/92 (100%)  
Strand = Plus / Plus

Query: 1 gaagagatgttcagggttttcggttatcggaatggatcgaaacttgattttctcatacttc 60  
|||||  
Sbjct: 2512 gaagagatgttcagggttttcggttatcggaatggatcgaaacttgattttctcatacttc 2571

Query: 61 tcgtcaggcgtggagtaacgcgcgccacggaa 92  
|||||  
Sbjct: 2572 tcgtcaggcgtggagtaacgcgcgccacggaa 2603

☐ >[gi|30043176|gb|AE016991.1|](#) ☒ Shigella flexneri 2a str. 2457T section 14 of 16 o  
Length = 293558

Score = 182 bits (92), Expect = 6e-44  
Identities = 92/92 (100%)  
Strand = Plus / Minus

```
Query: 1      gaagagatgttcagggttttcgttatcggaatggtatcgaacttgattttctcacttc 60
             |||
Sbjct: 117498 gaagagatgttcagggttttcgttatcggaatggtatcgaacttgattttctcacttc 117439
```

☐ >gi|2367266|gb|AE000447.1|AE000447 Escherichia coli K12 MG1655 section 337 of  
Length = 11355

```
Query: 1      gaagagatgttcagggttttcgttatcggaatggatcgaaacttgattttctcatacttc 60
              |||||
Sbjct: 8832   gaagagatgttcagggttttcgttatcggaatggatcgaaacttgattttctcatacttc 8773
```

☐ >gi|290484|gb|L10328.1|ECOW82 E. coli; the region from 81.5 to 84.5 minutes  
Length = 136254


Query: 1 gaagagatgttcagggttttcggtatcggaactggtatcggaactgtatttctcatacttc 60  
|||||  
Sbjct: 75216 gaagagatgttcagggttttcggtatcggaactggtatcggaactgtatttctcatacttc 75157

☐ >gi|12518536|gb|AE005601.1|AE005601  Escherichia coli O157:H7 EDL933 genome, co  
290  
Length = 11316

Query: 1 gaagagatgttcagggttttcggttatcggaatggtatcgaacttgatatttctcatacttc 60

|||||  
Sbjct: 8839 gaagagatgttcagggttttcgttatcggaatggtatcgaacttgatttctcgtaacttc 8780


Query: 61 tcgtcaggcgtggagtacgccgcgccacggaa 92  
|||||  
Sbjct: 8779 tcgtcaggcgtggagtacgccgcgccacggaa 8748

☐ >[gi|13363930|dbj|AF002566.1|](#)  Escherichia coli O157:H7 DNA, complete genome, se  
Length = 280900

Score = 174 bits (88), Expect = 1e-41  
Identities = 91/92 (98%)  
Strand = Plus / Minus

Query: 1 gaagagatgttcagggttttcgttatcggaatggtatcgaacttgatttctcataacttc 60  
|||||  
Sbjct: 185002 gaagagatgttcagggttttcgttatcggaatggtatcgaacttgatttctcgtaacttc 184943


Query: 61 tcgtcaggcgtggagtacgccgcgccacggaa 92  
|||||  
Sbjct: 184942 tcgtcaggcgtggagtacgccgcgccacggaa 184911

☐ >[gi|26110701|gb|AE016769.1|](#)  Escherichia coli CFT073 section 15 of 18 of the co  
Length = 301566

Score = 167 bits (84), Expect = 4e-39  
Identities = 90/92 (97%)  
Strand = Plus / Minus

Query: 1 gaagagatgttcagggttttcgttatcggaatggtatcgaacttgatttctcataacttc 60  
|||||  
Sbjct: 155271 gaagagatgttcagggttttcgttatcggaatggtatcgaacttgatttctcgtaacttc 155212

Query: 61 tcgtcaggcgtggagtacgccgcgccacggaa 92  
|||||  
Sbjct: 155211 tcgtcaggcgtggagtacgccgcgccacggaa 155180

☐ >[gi|29139451|gb|AE016846.1|](#)  Salmonella enterica subsp. enterica serovar Typhi  
of the complete genome  
Length = 300592

Score = 111 bits (56), Expect = 2e-22  
Identities = 74/80 (92%)  
Strand = Plus / Plus

Query: 13 aggttttcgttatcggaatggtatcgaacttgatttctcataacttctcgtaaggcgtg 72  
|||||

```
Query: 40      aacttgatatttctcatact 58
              |||
Sbjct: 37798  aacttgatatttctcatact 37816
```

☐ >gi|24202118|gb|AE011592.1| ☒ Leptospira interrogans serovar lai str. 56601 chro  
4 of 34 of the complete sequence  
Length = 10029

Score = 38.2 bits (19), Expect = 2.2  
Identities = 19/19 (100%)  
Strand = Plus / Plus

Query: 36 atcgaacttgatattctca 54  
|||||  
Sbjct: 1975 atcgaacttgatattctca 1993

☐ >gi|17739388|gb|AE009065.1|AE009065 ☒ Agrobacterium tumefaciens strain C58 circ  
256 of the complete sequence  
Length = 11490

Score = 38.2 bits (19), Expect = 2.2  
Identities = 19/19 (100%)  
Strand = Plus / Plus

Query: 47 atttctcatacttctcgtc 65  
|||||  
Sbjct: 11242 atttctcatacttctcgtc 11260

☐ >gi|15156031|gb|AE008032.1|AE008032 ☒ Agrobacterium tumefaciens str. C58 circula  
of 254 of the complete sequence  
Length = 10029


Score = 38.2 bits (19), Expect = 2.2  
Identities = 19/19 (100%)  
Strand = Plus / Plus

Query: 47 atttctcatacttctcgtc 65  
|||||  
Sbjct: 361 atttctcatacttctcgtc 379

☐ >gi|14193024|gb|AC013718.6| ☒ Homo sapiens BAC clone RP11-116I17 from 2, complet  
Length = 177855


Score = 38.2 bits (19), Expect = 2.2  
Identities = 19/19 (100%)  
Strand = Plus / Minus

Query: 55 tacttctcgtcaggcgtgg 73  
|||||  
Sbjct: 44290 tacttctcgtcaggcgtgg 44272

☐ >gi|19909496|gb|AC098742.4|  Mus musculus BAC clone RP23-122N2 from 14, complet  
Length = 218683


Score = 36.2 bits (18), Expect = 8.8  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 42     cttgtatttctcatactt 59  
             | | | | | | | | | | | | | | | |  
Sbjct: 93912 cttgtatttctcatactt 93929

☐ >gi|33147141|gb|AC144644.3|  Medicago truncatula clone mth2-1413, complete sequ  
Length = 117645


Score = 36.2 bits (18), Expect = 8.8  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 11     tcagggttttcggttatcg 28  
             | | | | | | | | | | | | | | | |  
Sbjct: 56388 tcagggttttcggttatcg 56405

☐ >gi|18642908|gb|AC080132.6|  Homo sapiens BAC clone RP11-166B20 from 4, complet  
Length = 114320

Score = 36.2 bits (18), Expect = 8.8  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 44     tgtatttctcatacttct 61  
             | | | | | | | | | | | | | | | |  
Sbjct: 100043 tgtatttctcatacttct 100026

☐ >gi|29243387|dbj|AF001011.6|  Homo sapiens genomic DNA, chromosome 18 clone:RP1  
sequence  
Length = 204777

Score = 36.2 bits (18), Expect = 8.8  
Identities = 21/22 (95%)  
Strand = Plus / Plus

Query: 41     acttgatttctcatacttctc 62  
             | | | | | | | | | | | | | | | |  
Sbjct: 27088 acttgatttctcatacttctc 27109





☐ >[gi|15128594|dbj|AB055625.1](#) ☒ Inversidens japonensis mitochondrial DNA, ND5 to  
haplotype:female type  
Length = 16826

Score = 36.2 bits (18), Expect = 8.8  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 42 cttgtattttctcatactt 59  
|||||  
Sbjct: 2522 cttgtattttctcatactt 2505

☐ >[gi|14043054|emb|AL450324.10](#) ☒ Human DNA sequence from clone RP11-307F22 on chr  
sequence  
Length = 101846

Score = 36.2 bits (18), Expect = 8.8  
Identities = 21/22 (95%)  
Strand = Plus / Minus

Query: 40 aacttgattttctcatacttct 61  
|||||  
Sbjct: 13663 aacttttattttctcatacttct 13642